

SEQUENCE LISTING

<110> Kobilka, Brian K.
Ghanouni, Pejman
Lee, Tae Weon

<120> Conformational assays to detect binding
to membrane spanning, signal-transducing proteins

<130> STAN-213CIP

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<141> 2003-10-22

<150> PCT/US02/13250
<151> 2002-04-24

<150> 09/935,061
<151> 2001-08-21

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1 5 10 15	

agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg	96
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp	
20 25 30	

gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg	144
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val	
35 40 45	

ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg	192
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu	
50 55 60	

cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg	240
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu	
65 70 75 80	

gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc gcc cat att ctt atg	288
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met	
85 90 95	

aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att	336
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile	
100 105 110	

gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca	384
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala	
115 120 125	

gtg gat cgc tac ttt gcc att act tca cct ttc aag tac cag agc ctg Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu	432
130 135 140	
ctg acc aag aat aag gcc cggtg atc att ctg atg gtg tgg att gtg Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val	480
145 150 155 160	
tca ggc ctt acc tcc ttc ttg ccc att cag atg cac tgg tac cggtt Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala	528
165 170 175	
acc cac cag gaa gcc atc aac tgc tat gcc aat gag acc tgc tgc gac Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp	576
180 185 190	
ttc ttc acg aac caa gcc tat gcc att gcc tct tcc atc gtg tcc ttc Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe	624
195 200 205	
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210 215 220	
gag gcc aaa agg cag ctc cag aag att gac aaa tct gag ggc cgc ttc Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe	720
225 230 235 240	
cat gtc cag aac ctt agc cag gtg gag cag gat ggg cggtt acg ggg cat His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His	768
245 250 255	
gga ctc cgc aga tct tcc aag ttc tgc ttg aag gag cac aaa gcc ctc Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu	816
260 265 270	
aag acg tta ggc atc atc atg ggc act ttc acc ctc tgc tgg ctg ccc Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro	864
275 280 285	
ttc ttc atc gtt aac att gtg cat gtg atc cag gat aac ctc atc cgt Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg	912
290 295 300	
aag gaa gtt tac atc ctc cta aat tgg ata ggc tat gtc aat tct ggt Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly	960
305 310 315 320	
ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc agg att gcc ttc Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe	1008
325 330 335	
cag gag ctc ctg tgc ctg cgc agg tct tct ttg aag gcc tat ggg aat Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn	1056
340 345 350	
ggc tac tcc agc aac ggc aac aca ggg gag cag agt gga tat cac gtg Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val	1104
355 360 365	

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 370 375 380
 gaa gac ttt gtg ggc cat caa ggt act gtg cct agc gat aac att gat 1200
 Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp
 385 390 395 400
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 Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val 35 40 45
 Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu 50 55 60
 Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu 65 70 75 80
 Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met 85 90 95
 Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile 100 105 110
 Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala 115 120 125
 Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu 130 135 140
 Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val 145 150 155 160
 Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala 165 170 175
 Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp. 180 185 190
 Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe 195 200 205
 Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln 210 215 220
 Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe 225 230 235 240
 His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His 245 250 255
 Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala. Leu 260 265 270
 Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro 275 280 285
 Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg 290 295 300
 Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly

305	310	315	320
Phe Asn Pro Leu Ile Tyr Cys Arg Ser	Pro Asp Phe Arg Ile Ala Phe		
325	330	335	
Gln Glu Leu Leu Cys Leu Arg Arg Ser	Ser Leu Lys Ala Tyr Gly Asn		
340	345	350	
Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val			
355	360	365	
Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr			
370	375	380	
Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp			
385	390	395	400
Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu			
405	410		

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<211> 1239

<212> DNA

<213> Artificial Sequence

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<223> Beta-2 Adrenergic Receptor with TEV site in 2nd
intracellular loop

<221> CDS

<222> (1)...(1239)

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Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg			
1	5	10	15

agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg	96		
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp			
20	25	30	

gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg	144		
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val			
35	40	45	

ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg	192		
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu			
50	55	60	

cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg	240		
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu			
65	70	75	80

gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc cat att ctt atg	288		
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met			
85	90	95	

aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att	336		
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile			
100	105	110	

gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca	384		
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala			
115	120	125	

gtg gat cgc tac ttt gcc att act tca cct ttc aag tac cag agc ctg Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu	130 135 140	432
ctg acc aag aat aag gcc cggtg atc att ctg atg gtg tgg att gtg Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val	145 150 155 160	480
tca ggc ctt acc tcc ttc ttg ccc att cag atg cac tgg tac cgg gcc Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala	165 170 175	528
acc cac cag gaa gcc atc aac tgc tat gcc aat gag acc tgc tgt gac Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp	180 185 190	576
ttc ttc acg aac caa gcc tat gcc att gcc tct tcc atc gtg tcc ttc Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe	195 200 205	624
tac gtt ccc ctg gtg atc atg gtc ttc gtc tac tcc agg gtc ttt cag Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln	210 215 220	672
gag gcc aaa agg cag ctc cag aag att gac aaa tct gag ggc cgc ttc Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe	225 230 235 240	720
cat gtc cag aac ctt agc cag gtg gag cag gat ggg cggtt acg ggg cat His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His	245 250 255	768
gga ctc gaa aac ctc tac ttc cag ggg ttg aag gag cac aaa gcc ctc Gly Leu Glu Asn Leu Tyr Phe Gln Gly Leu Lys Glu His Lys Ala Leu	260 265 270	816
aag acg tta ggc atc atc atg ggc act ttc acc ctc tgc tgg ctg ccc Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro	275 280 285	864
ttc ttc atc aac att gtg cat gtg atc cag gat aac ctc atc cgt Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg	290 295 300	912
aag gaa gtt tac atc ctc cta aat tgg ata ggc tat gtc aat tct ggt Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly	305 310 315 320	960
ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc agg att gcc ttc Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe	325 330 335	1008
cag gag ctc ctg tgc ctg cgc agg tct ttc ttg aag gcc tat ggg aat Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn	340 345 350	1056
ggc tac tcc agc aac ggc aac aca ggg gag cag agt gga tat cac gtg Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val	355 360 365	1104

gaa cag gag aaa gaa aat aaa ctg ctg tgt gaa gac ctc cca ggc acg .. 1152
Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr
370 375 380

gaa gac ttt gtg ggc cat caa ggt act gtg cct agc gat aac att gat 1200
Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp
385 390 395 400

tca caa ggg agg aat tgt agt aca aat gac tca ctg ctg 1239
Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
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<211> 413

<212> PRT

<213> Artificial Sequence

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<223> Beta-2 Adrenergic Receptor with TEV site in 2nd
intracellular loop

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Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
20 25 30

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35 40 45

Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
50 55 60

Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
65 70 75 80

Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
85 90 95

Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
100 105 110

Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
115 120 125

Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
130 135 140

Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val
145 150 155 160

Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
165 170 175

Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
180 185 190

Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
195 200 205

Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln
210 215 220

Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
225 230 235 240

His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His
245 250 255

Gly Leu Glu Asn Leu Tyr Phe Gln Gly Leu Lys Glu His Lys Ala Leu
260 265 270

Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro

	275	280	285
Phe	Phe Ile Val Asn Ile Val His	Val Ile Gln Asp	Asn Leu Ile Arg
290	295	300	
Lys	Glu Val Tyr Ile Leu Leu Asn Trp	Ile Gly Tyr Val Asn Ser Gly	
305	310	315	320
Phe	Asn Pro Leu Ile Tyr Cys Arg Ser	Pro Asp Phe Arg Ile Ala Phe	
	325	330	335
Gln	Glu Leu Leu Cys Leu Arg Arg Ser	Ser Leu Lys Ala Tyr Gly Asn	
	340	345	350
Gly	Tyr Ser Ser Asn Gly Asn Thr	Gly Glu Gln Ser Gly Tyr His Val	
	355	360	365
Glu	Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr		
	370	375	380
Glu	Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp		
385	390	395	400
Ser	Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu		
	405	410	

<210> 9

<211> 1251

<212> DNA

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<223> Beta-2 Adrenergic Receptor with TEV site in 3rd intracellular loop

<221> CDS

<222> (1)...(1251)

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48

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agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
                    20          25          30

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96

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gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
          .   35           40           45

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144

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ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
      50           55           60

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192

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cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
   65           70           75           80

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240

gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc gcc cat att ctt atg
 Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
 85 90 · 95

288

aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
100 105 110

336

gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala 115	120	125	384	
gtg gat cgc tac ttt gcc att act tca cct ttc aag gag aat ctc tac Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Glu Asn Leu-Tyr 130	135	140	432	
ttc cag ggc ctg ctg acc aag aat aag gcc cggtc att ctg atg Phe Gln Gly Leu Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met 145	150	155	160	480
gtg tgg att gtg tca ggc ctt acc tcc ttc ttg ccc att cag atg cac Val Trp Ile Val Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His 165	170	175	528	
tgg tac cgg gcc acc cac cag gaa gcc atc aac tgc tat gcc aat gag Trp Tyr Arg Ala Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu 180	185	190	576	
acc tgc tgt gac ttc ttc acg aac caa gcc tat gcc att gcc tct tcc Thr Cys Cys Asp Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser 195	200	205	624	
atc gtg tcc ttc tac gtt ccc ctg gtg atc atg gtc ttc gtc tac tcc Ile Val Ser Phe Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser 210	215	220	672	
agg gtc ttt cag gag gcc aaa agg cag ctc cag aag att gac aaa tct Arg Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser 225	230	235	240	720
gag ggc cgc ttc cat gtc cag aac ctt agc cag gtg gag cag gat ggg Glu Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly 245	250	255	768	
cgg acg ggg cat gga ctc cgc aga tct tcc aag ttc tgc ttg aag gag Arg Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu 260	265	270	816	
cac aaa gcc ctc aag acg tta ggc atc atc atg ggc act ttc acc ctc His Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu 275	280	285	864	
tgc tgg ctg ccc ttc atc gtt aac att gtg cat gtg atc cag gat Cys Trp Leu Pro Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp 290	295	300	912	
aac ctc atc cgt aag gaa gtt tac atc ctc cta aat tgg ata ggc tat Asn Leu Ile Arg Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr 305	310	315	320	960
gtc aat tct ggt ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc Val Asn Ser Gly Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe 325	330	335	1008	
agg att gcc ttc cag gag ctc ctg tgc ctg cgc agg tct tct ttg aag Arg Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys 340	345	350	1056	

gcc tat ggg aat ggc tac tcc .agc aac ggc aac aca ggg gag cag agt		1104	
Ala Tyr Gly Asn Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser			
355	360	365	
gga tat cac gtg gaa cag gag aaa gaa aat aaa ctg ctg tgt gaa gac		1152	
Gly Tyr His Val Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp			
370	375	380	
ctc cca ggc acg gaa gac ttt gtg ggc cat caa ggt act gtg cct agc		1200	
Leu Pro Gly Thr Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser			
385	390	395	400
gat aac att gat tca caa ggg agg aat tgt agt aca aat gac tca ctg		1248	
Asp Asn Ile Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu			
405	410	415	
ctg		1251	
Leu			

<210> 10
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<212> PRT
<213> Artificial Sequence

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<223> Beta-2 Adrenergic Receptor with TEV site in 3rd
intracellular loop

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1	5	10	15
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp			
20	25	30	
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val			
35	40	45	
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu			
50	55	60	
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu			
65	70	75	80
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met			
85	90	95	
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile			
100	105	110	
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala			
115	120	125	
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Glu Asn Leu Tyr			
130	135	140	
Phe Gln Gly Leu Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met			
145	150	155	160
Val Trp Ile Val Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His			
165	170	175	
Trp Tyr Arg Ala Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu			
180	185	190	
Thr Cys Cys Asp Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser			
195	200	205	
Ile Val Ser Phe Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser			

210	215	220
Arg Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser		
225	230	235 240
Glu Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly		
245	250	255
Arg Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu		
260	265	270
His Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu		
275	280	285
Cys Trp Leu Pro Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp		
290	295	300
Asn Leu Ile Arg Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr		
305	310	315 320
Val Asn Ser Gly Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe		
325	330	335
Arg Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys		
340	345	350
Ala Tyr Gly Asn Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser		
355	360	365
Gly Tyr His Val Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp		
370	375	380
Leu Pro Gly Thr Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser		
385	390	395 400
Asp Asn Ile Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu		
405	410	415
Leu		

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<212> DNA
<213> homo sapiens

<220>
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<222> (1)...(1176)

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atg gac agc agc gct gcc ccc acg aac gcc agc aat tgc act gat gcc		48
Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala		
1	5	10
		15
ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc		96
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val		
20	25	30
aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac		144
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn		
35	40	45
cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt		192
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser		
50	55	60
ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg		240
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val		
65	70	75
		80
tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc		288

Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val			
85	90	95	
aga tac acc aag atg aag act gcc acc aac atc tac att ttc aac ctt			336
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu			
100	105	110	
gct ctg gca gat gcc tta gcc acc agt acc ctg ccc ttc cag agt gtg			384
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val			
115	120	125	
aat tac cta atg gga aca tgg cca ttt gga acc atc ctt tgc aag ata			432
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile			
130	135	140	
gtg atc tcc ata gat tac tat aac atg ttc acc agc ata ttc acc ctc			480
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu			
145	150	155	160
tgc acc atg agt gtt gat cga tac att gca gtc tgc cac cct gtc aag			528
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys			
165	170	175	
gcc tta gat ttc cgt act ccc cga aat gcc aaa att atc aat gtc tgc			576
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys			
180	185	190	
aac tgg atc ctc tct tca gcc att ggt ctt cct gta atg ttc ata gct			624
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala			
195	200	205	
aca aca aaa tac agg caa ggt tcc ata gat tgt aca cta aca ttc tct			672
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser			
210	215	220	
cat cca acc tgg tac tgg gaa aac ctg ctg aag atc tgt gtt ttc atc			720
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile			
225	230	235	240
ttc gcc ttc att atg cca gtg ctc atc att acc gtg tgc tat gga ctg			768
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu			
245	250	255	
atg atc ttg cgc ctc aag agt gtc cgc atg ctc tct ggc tcc aaa gaa			816
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu			
260	265	270	
aag gac agg aat ctt cga agg atc acc agg atg gtg ctg gtg gtg gtg			864
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val			
275	280	285	
gct gtg ttc atc gtc tgc tgg act ccc att cac att tac gtc atc att			912
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile			
290	295	300	
aaa gcc ttg gtt aca atc cca gaa act acg ttc cag act gtt tct tgg			960
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phé Gln Thr Val Ser Trp			
305	310	315	320

cac ttc tgc att gct cta ggt tac aca aac agc tgc ctc aac cca gtc His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val	325	330	335	1008
ctt tat gca ttt ctg gat gaa aac ttc aaa cga tgc ttc aga gag ttc Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe	340	345	350	1056
tgt atc cca acc tct tcc aac att gag caa caa aac tcc act cga att Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile	355	360	365	1104
cgt cag aac act aga gac cac ccc tcc acg gcc aat aca gtg gat aga Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg	370	375	380	1152
act aat cat cag gta cgc agt ctc Thr Asn His Gln Val Arg Ser Leu	385	390		1176
<210> 12				
<211> 392				
<212> PRT				
<213> homo sapiens				
<400> 12				
Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala	1	5	10	15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val	20	25	30	
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn	35	40	45	
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser	50	55	60	
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val	65	70	75	80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val	85	90	95	
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu	100	105	110	
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val	115	120	125	
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile	130	135	140	
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu	145	150	155	160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys	165	170	175	
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys	180	185	190	
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala	195	200	205	
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser	210	215	220	
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile	225	230	235	240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu	245	250	255	

Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glut
			260					265						270	
Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val
			275					280					285		
Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Tyr	Val	Ile	Ile
			290			295		.			300				
Lys	Ala	Leu	Val	Thr	Ile	Pro	Glu	Thr	Thr	Phe	Gln	Thr	Val	Ser	Trp
			305			310				315					320
His	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Cys	Leu	Asn	Pro	Val
						325			330					335	
Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Glu	Phe
								340		345				350	
Cys	Ile	Pro	Thr	Ser	Ser	Asn	Ile	Glu	Gln	Gln	Asn	Ser	Thr	Arg	Ile
								355		360			365		
Arg	Gln	Asn	Thr	Arg	Asp	His	Pro	Ser	Thr	Ala	Asn	Thr	Val	Asp	Arg
								370		375			380		
Thr	Asn	His	Gln	Val	Arg	Ser	Leu								
							385			390					

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<210> 13
<211> 1176
<212> DNA
<213> Artificial Sequence
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<220>
<223> ' Opioid receptor with TEV site in 2nd
intracellular loop

<221> CDS
<222> (1) ... (1176)

<400> 13
atg gac agc agc gct gcc ccc acg aac gcc agc aat tgc act gat gcc 48
Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15

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ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc      96
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
                         20          25          30

```

```

aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac      144
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn
          35           40           45

```

cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt . 192
 Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
 50 55 60

ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg 240
 Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
 65 . 70 75 80

tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc 288
 Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
 85 90 95

```

aga tac acc aag atg aag act gcc acc aac atc tac att ttc aac ctt      336
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
          100       .        105           110

```

gct ctg gca gat gcc tta gcc acc agt acc ctg ccc ttc cag agt gtg Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val 115 120 125	384
aat tac cta atg gga aca tgg cca ttt gga acc atc ctt tgc aag ata Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile 130 135 140	432
gtg atc tcc ata gat tac tat aac atg ttc acc agc ata ttc acc ctc Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu 145 150 155 160	480
tgc acc atg agt gtt gat cga tac att gca gtc tgc cac cct gtc aag Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys 165 170 175	528
gaa aac ctc tac ttc cag ggg cga aat gcc aaa att atc aat gtc tgc Glu Asn Leu Tyr Phe Gln Gly Arg Asn Ala Lys Ile Ile Asn Val Cys 180 185 190	576
aac tgg atc ctc tct tca gcc att ggt ctt cct gta atg ttc ata gct Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala 195 200 205	624
aca aca aaa tac agg caa ggt tcc ata gat tgt aca cta aca ttc tct Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser 210 215 220	672
cat cca acc tgg tac tgg gaa aac ctg ctg aag atc tgt gtt ttc atc His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile 225 230 235 240	720
ttc gcc ttc att atg cca gtg ctc atc att acc gtg tgc tat gga ctg Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu 245 250 255	768
atg atc ttg cgc ctc aag agt gtc cgc atg ctc tct ggc tcc aaa gaa Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu 260 265 270	816
aag gac agg aat ctt cga agg atc acc agg atg gtg ctg gtg gtg gtg Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val 275 280 285	864
gct gtg ttc atc gtc tgc tgg act ccc att cac att tac gtc atc att Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile 290 295 300	912
aaa gcc ttg gtt aca atc cca gaa act acg ttc cag act gtt tct tgg Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp 305 310 315 320	960
cac ttc tgc att gct cta ggt tac aca aac agc tgc ctc aac cca gtc His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val 325 330 335	1008
ctt tat gca ttt ctg gat gaa aac ttc aaa cga tgc ttc aga gag ttc Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe	1056

340

345

350

tgt atc cca acc tct tcc aac att gag caa caa aac tcc act cga att			1104
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile			
355	360	365	

cgt cag aac act aga gac cac ccc tcc acg gcc aat aca gtg gat aga			1152
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg			
370	375	380	

act aat cat cag gta cgc agt ctc			1176
Thr Asn His Gln Val Arg Ser Leu			
385	390		

<210> 14
<211> 392
<212> PRT
<213> Artificial Sequence

<220>
<223> ' Opioid receptor with TEV site in 2nd
intracellular loop

<400> 14			
Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala			
1	5	10	15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val			
20	25	30	
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn			
35	40	45	
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser			
50	55	60	
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val			
65	70	75	80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val			
85	90	95	
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu			
100	105	110	
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val			
115	120	125	
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile			
130	135	140	
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu			
145	150	155	160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys			
165	170	175	
Glu Asn Leu Tyr Phe Gln Gly Arg Asn Ala Lys Ile Ile Asn Val Cys			
180	185	190	
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala			
195	200	205	
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser			
210	215	220	
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile			
225	230	235	240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu			
245	250	255	
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu			
260	265	270	

Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
 275 280 285
 Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
 290 295 300
 Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
 305 310 315 320
 His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
 325 330 335
 Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
 340 345 350
 Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
 355 360 365
 Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
 370 375 380
 Thr Asn His Gln Val Arg Ser Leu
 385 390

<210> 15

<211> 1197

<212> DNA

<213> Artificial Sequence

<220>

<223> ' Opioid receptor with TEV site in 3rd
intracellular loop

<221> CDS

<222> (1)...(1197)

<400> 15

atg gac agc agc gct gcc ccc acg aac gcc agc aat tgc act gat gcc	48
Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala	
1 5 10 15	

ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc	96.
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val	
20 25 30	

aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac	144
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn	
35 40 45	

cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt	192
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser	
50 55 60	

ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg	240
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val	
65 70 75 80	

tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc	288
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val	
85 90 95	

aga tac acc aag atg aag act gcc acc aac atc tac att ttc aac ctt	336
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu	
100 105 110	

gct ctg gca gat gcc tta gcc acc agt acc ctg ccc ttc cag agt gtg	384
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Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val			
115	120	125	
aat tac cta atg gga aca tgg cca ttt gga acc atc ctt tgc aag ata			432
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile			
130	135	140	
gtg atc tcc ata gat tac tat aac atg ttc acc agc ata ttc acc ctc			480
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu			
145	150	155	160
tgc acc atg agt gtt gat cga tac att gca gtc tgc cac cct gtc aag			528
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys			
165	170	175	
gcc tta gat ttc cgt act ccc cga aat gcc aaa att atc aat gtc tgc			576
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys			
180	185	190	
aac tgg atc ctc tct tca gcc att ggt ctt cct gta atg ttc ata gct			624
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala			
195	200	205	
aca aca aaa tac agg caa ggt tcc ata gat tgt aca cta aca ttc tct			672
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser			
210	215	220	
cat cca acc tgg tac tgg gaa aac ctg ctg aag atc tgt gtt ttc atc			720
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile			
225	230	235	240
ttc gcc ttc att atg cca gtg ctc atc att acc gtg tgc tat gga ctg			768
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu			
245	250	255	
atg atc ttg cgc ctc aag agt gtc cgc atg ctc tct ggc tcc aaa gaa			816
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu			
260	265	270	
aag gac gaa aac ctc tac ttc cag ggg agg aat ctt cga agg atc acc			864
Lys Asp Glu Asn Leu Tyr Phe Gln Gly Arg Asn Leu Arg Arg Ile Thr			
275	280	285	
agg atg gtg ctg gtg gtg gct gtg ttc atc gtc tgc tgg act ccc			912
Arg Met Val Leu Val Val Ala Val Phe Ile Val Cys Trp Thr Pro			
290	295	300	
att cac att tac gtc atc att aaa gcc ttg gtt aca atc cca gaa act			960
Ile His Ile Tyr Val Ile Ile Lys Ala Leu Val Thr Ile Pro Glu Thr			
305	310	315	320
acg ttc cag act gtt tct tgg cac ttc tgc att gct cta ggt tac aca			1008
Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile Ala Leu Gly Tyr Thr			
325	330	335	
aac agc tgc ctc aac cca gtc ctt tat gca ttt ctg gat gaa aac ttc			1056
Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe			
340	345	350	

aaa cga tgc ttc aga gag ttc tgt atc cca acc tct tcc aac att gag		1104
Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Asn Ile Glu		
355	360	365
caa caa aac tcc act cga att cgt cag aac act aga gac cac ccc tcc		1152
Gln Gln Asn Ser Thr Arg Ile Arg Gln Asn Thr Arg Asp His Pro Ser		
370	375	380
acg gcc aat aca gtg gat aga act aat cat cag gta cgc agt ctc		1197
Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Val Arg Ser Leu		
385	390	395
<210> 16		
<211> 399		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> ' Opioid receptor with TEV site in 3rd		
intracellular loop		
<400> 16		
Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala		
1 5 10 15		
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val		
20 25 30		
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn		
35 40 45		
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser		
50 55 60		
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val		
65 70 75 80		
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val		
85 90 95		
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu		
100 105 110		
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val		
115 120 125		
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile		
130 135 140		
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu		
145 150 155 160		
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys		
165 170 175		
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys		
180 185 190		
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala		
195 200 205		
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser		
210 215 220		
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile		
225 230 235 240		
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu		
245 250 255		
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu		
260 265 270		
Lys Asp Glu Asn Leu Tyr Phe Gln Gly Arg Asn Leu Arg Arg Ile Thr		
275 280 285		

Arg Met Val Leu Val Val Ala Val Phe Ile Val Cys Trp Thr Pro
290 295 300
Ile His Ile Tyr Val Ile Ile Lys Ala Leu Val Thr Ile Pro Glu Thr
305 310 315 320
Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile Ala Leu Gly Tyr Thr
325 330 335
Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe
340 345 350
Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Asn Ile Glu
355 360 365
Gln Gln Asn Ser Thr Arg Ile Arg Gln Asn Thr Arg Asp His Pro Ser
370 375 380
Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Val Arg Ser Leu
385 390 395

<210> 17

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Hemagglutinin tag

<400> 17

Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5 10

<210> 18

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> c-myc tag

<400> 18

Cys Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 19

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> enterokinase cleavage site

<400> 19

Asp Asp Asp Asp Lys
1 5

<210> 20

<211> 4

<212> PRT

<213> Artificial Sequence

<220>
<223> factor Xa cleavage site

<400> 20
Ile Glu Gly Arg
1

<210> 21
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> thrombin cleavage site

<400> 21
Leu Val Pro Ala Gly Ser
1 5

<210> 22
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> renin cleavage site

<400> 22
His Pro Phe His Leu Val Ile His
1 5